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<150> 00201871.1

<151> 2000-05-25

<160> 9

<170> PatentIn Ver. 2.1

<210> 1

<211> 6026

<212> DNA

<213> Lactobacillus reuteri

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<221> RBS

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Glu Leu Asn His Tyr Ser Glu Ile Val Gln Gln Asn Ile Glu Lys Arg	
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1180

1185

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Phe Ile Glu Asp Ser Val Gly Asn Trp Tyr Phe Phe Asp Gln Asp Gly	
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Met Val Arg Asn Gln Thr Ile Asn Ala Gly Ala Met Ile Tyr Thr Leu	
1735 1740 1745	
gat gaa aac ggt aag ctt ata aag gct agt tat aat tca gat gcc gaa	5455
Asp Glu Asn Gly Lys Leu Ile Lys Ala Ser Tyr Asn Ser Asp Ala Glu	
1750 1755 1760 1765	
tat cca act tca act gat gtt ggt aag atg ctt gat caa aat aaa cta	5503
Tyr Pro Thr Ser Thr Asp Val Gly Lys Met Leu Asp Gln Asn Lys Leu	
1770 1775 1780	
taa atggaaataa ttagctgatt tccgtttctt agaatcgaaa gatttaataa	5556
ctgggggttaa aacggcccta caaaatctga tattgatata gagatattat ttcctatatc	5616
aatatcagat ttttgctttt tataaaattg attgtgacta ataagaatcc ggaagataac	5676
gttggttgta tatcagtggg ttttaagcaac atgaattaat tgaagatgac ggcaatgatt	5736
aaaagtcggt ctgatgatta ttgatgtatt actagtattt ggttttttatc atttatattt	5796
ttactgttat tgggtgtcata tattccacaa taacagtaaa ggtatatatg ctagttttatt	5856
ttttaagtaa ttataatatt ctgattataa tttggaaata ttcgctttta gcaaaaaggt	5916
agtaaacaga tcagaatcgt cattctgctt ttctactact aaaagtctgt tttaaattct	5976
aaactaaaat aggctaaaca ctgatgttta tcatttatat ttttactgtt	6026

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<211> 1781
 <212> PRT
 <213> Lactobacillus reuteri

<400> 2

Met	Glu	Ile	Lys	Lys	His	Phe	Lys	Leu	Tyr	Lys	Ser	Gly	Lys	Gln	Trp
1				5					10					15	
Val	Thr	Ala	Ala	Val	Ala	Thr	Val	Ala	Val	Ser	Thr	Ala	Leu	Leu	Tyr
			20					25					30		
Gly	Gly	Val	Ala	His	Ala	Asp	Gln	Gln	Val	Gln	Gln	Ala	Ser	Thr	Thr
		35					40					45			
Gln	Asp	Gln	Thr	Ser	Thr	Val	Asn	Asn	Asp	Thr	Asp	Lys	Thr	Val	Ala
	50					55					60				
Leu	Asp	Thr	Asn	Thr	Asp	Gln	Ser	Ala	Gln	Thr	Thr	Asp	Lys	Lys	Gln
	65				70					75					80
Val	Val	Ser	Asn	Thr	Asn	Gln	Ser	Lys	Thr	Asp	Asp	Thr	Ser	Thr	Ala
				85					90					95	
Asp	Lys	Asn	Ser	Thr	Ser	Thr	Pro	Val	Ser	Val	Leu	Pro	Ser	Asn	Asn
			100					105					110		
Thr	Glu	Lys	Gln	Ala	Lys	Asn	Tyr	Asn	Glu	Gln	Asp	Lys	Gly	Asn	Tyr
		115					120					125			
Gly	Asn	Ile	Asp	Thr	Ala	Tyr	Phe	Ser	Asn	Asn	Gln	Leu	His	Val	Ser
	130					135					140				
Gly	Trp	Asn	Ala	Thr	Asn	Ala	Ser	Gln	Gly	Thr	Asn	Ser	Arg	Gln	Ile
	145				150					155					160
Ile	Val	Arg	Asp	Ile	Thr	Thr	Asn	Asn	Glu	Leu	Gly	Arg	Thr	Asp	Val
			165						170					175	
Thr	Asn	Asn	Val	Ala	Arg	Pro	Asp	Val	Lys	Asn	Val	His	Asn	Val	Tyr
			180					185					190		
Asn	Ala	Asp	Asn	Ser	Gly	Phe	Asp	Val	Asn	Val	Asn	Ile	Asp	Phe	Ser
		195					200					205			
Lys	Met	Lys	Asp	Tyr	Arg	Asp	Ser	Ile	Glu	Ile	Val	Ser	Arg	Tyr	Ser
	210					215					220				
Gly	Asn	Gly	Lys	Ser	Val	Asp	Trp	Trp	Ser	Gln	Pro	Ile	Thr	Phe	Asp
	225				230					235					240
Lys	Asn	Asn	Tyr	Ala	Tyr	Leu	Asp	Thr	Phe	Glu	Val	Lys	Asn	Gly	Glu
				245					250					255	
Leu	His	Ala	Thr	Gly	Trp	Asn	Ala	Thr	Asn	Ser	Ala	Ile	Asn	Tyr	Asn
			260					265					270		
His	His	Phe	Val	Ile	Leu	Phe	Asp	Gln	Thr	Asn	Gly	Lys	Glu	Val	Ala

275

280

285

Arg Gln Glu Val Arg Glu Gly Gln Ser Arg Pro Asp Val Ala Lys Val
290 295 300

Tyr Pro Gln Val Val Gly Ala Ala Asn Ser Gly Phe Asn Val Thr Phe
305 310 315 320

Asn Ile Ser Asp Leu Asp Tyr Thr His Gln Tyr Gln Val Leu Ser Arg
325 330 335

Tyr Ser Asn Ser Asp Asn Gly Glu Gly Asp Asn Val Thr Tyr Trp Phe
340 345 350

Asn Pro Gln Ser Ile Ala Pro Ala Asn Gln Ser Asn Gln Gly Tyr Leu
355 360 365

Asp Ser Phe Asp Ile Ser Lys Asn Gly Glu Val Thr Val Thr Gly Trp
370 375 380

Asn Ala Thr Asp Leu Ser Glu Leu Gln Asn Asn His Tyr Val Ile Leu
385 390 395 400

Phe Asp Gln Thr Ala Gly Lys Gln Val Ala Ser Ala Lys Ala Asp Leu
405 410 415

Ile Ser Arg Pro Asp Val Ala Lys Ala Tyr Pro Thr Val Lys Thr Ala
420 425 430

Thr Asn Ser Gly Phe Lys Val Thr Phe Lys Val Asn Asn Leu Gln Pro
435 440 445

Gly His Gln Tyr Ser Val Val Ser Arg Phe Ser Ala Asp Glu Asn Gly
450 455 460

Asn Gly Asn Asp Lys Arg His Thr Asp Tyr Trp Phe Ser Pro Val Ile
465 470 475 480

Leu Asn Gln Thr Ala Ser Asn Ile Asp Thr Ile Thr Met Thr Ser Asn
485 490 495

Gly Leu His Ile Ala Gly Trp Met Ala Ser Asp Asn Ser Ile Asn Glu
500 505 510

Thr Thr Pro Tyr Ala Ile Ile Leu Asn Asn Gly Lys Glu Val Thr Arg
515 520 525

Gln Lys Met Ser Leu Thr Ala Arg Pro Asp Val Ala Ala Val Tyr Pro
530 535 540

Ser Leu Tyr Asn Ser Ala Val Ser Gly Phe Asp Thr Thr Ile Lys Leu
545 550 555 560

Thr Asn Asp Gln Tyr Gln Ala Leu Asn Gly Gln Leu Gln Val Leu Leu
565 570 575

Arg Phe Ser Lys Ala Ala Asp Gly Asn Pro Ser Gly Asp Asn Thr Val

580

585

590

Thr Asp Gln Phe Ser Lys Asn Tyr Ala Thr Thr Gly Gly Asn Phe Asp
595 600 605

Tyr Val Lys Val Asn Gly Asn Gln Val Glu Phe Ser Gly Trp His Ala
610 615 620

Thr Asn Gln Ser Asn Asp Lys Asp Ser Gln Trp Ile Ile Val Leu Val
625 630 635 640

Asn Gly Lys Glu Val Lys Arg Gln Leu Val Asn Asp Thr Lys Glu Gly
645 650 655

Ala Ala Gly Phe Asn Arg Asn Asp Val Tyr Lys Val Asn Pro Ala Ile
660 665 670

Glu Asn Ser Ser Met Ser Gly Phe Gln Gly Ile Ile Thr Leu Pro Val
675 680 685

Thr Val Lys Asn Glu Asn Val Gln Leu Val His Arg Phe Ser Asn Asp
690 695 700

Val Lys Thr Gly Glu Gly Asn Tyr Val Asp Phe Trp Ser Glu Leu Met
705 710 715 720

Pro Val Lys Asp Ser Phe Gln Lys Gly Asn Gly Pro Leu Lys Gln Phe
725 730 735

Gly Leu Gln Thr Ile Asn Gly Gln Gln Tyr Tyr Ile Asp Pro Thr Thr
740 745 750

Gly Gln Pro Arg Lys Asn Phe Leu Leu Gln Ser Gly Asn Asn Trp Ile
755 760 765

Tyr Phe Asp Ser Asp Thr Gly Val Gly Thr Asn Ala Leu Glu Leu Gln
770 775 780

Phe Ala Lys Gly Thr Val Ser Ser Asn Glu Gln Tyr Arg Asn Gly Asn
785 790 795 800

Ala Ala Tyr Ser Tyr Asp Asp Lys Ser Ile Glu Asn Val Asn Gly Tyr
805 810 815

Leu Thr Ala Asp Thr Trp Tyr Arg Pro Lys Gln Ile Leu Lys Asp Gly
820 825 830

Thr Thr Trp Thr Asp Ser Lys Glu Thr Asp Met Arg Pro Ile Leu Met
835 840 845

Val Trp Trp Pro Asn Thr Leu Thr Gln Ala Tyr Tyr Leu Asn Tyr Met
850 855 860

Lys Gln His Gly Asn Leu Leu Pro Ser Ala Leu Pro Phe Phe Asn Ala
865 870 875 880

Asp Ala Asp Pro Ala Glu Leu Asn His Tyr Ser Glu Ile Val Gln Gln

885

890

895

Asn Ile Glu Lys Arg Ile Ser Glu Thr Gly Asn Thr Asp Trp Leu Arg
900 905 910

Thr Leu Met His Asp Phe Val Thr Asn Asn Pro Met Trp Asn Lys Asp
915 920 925

Ser Glu Asn Val Asn Phe Ser Gly Ile Gln Phe Gln Gly Gly Phe Leu
930 935 940

Lys Tyr Glu Asn Ser Asp Leu Thr Pro Tyr Ala Asn Ser Asp Tyr Arg
945 950 955 960

Leu Leu Gly Arg Met Pro Ile Asn Ile Lys Asp Gln Thr Tyr Arg Gly
965 970 975

Gln Glu Phe Leu Leu Ala Asn Asp Ile Asp Asn Ser Asn Pro Val Val
980 985 990

Gln Ala Glu Gln Leu Asn Trp Leu Tyr Tyr Leu Leu Asn Phe Gly Thr
995 1000 1005

Ile Thr Ala Asn Asn Asp Gln Ala Asn Phe Asp Ser Val Arg Val Asp
1010 1015 1020

Ala Pro Asp Asn Ile Asp Ala Asp Leu Met Asn Ile Ala Gln Asp Tyr
1025 1030 1035 1040

Phe Asn Ala Ala Tyr Gly Met Asp Ser Asp Ala Val Ser Asn Lys His
1045 1050 1055

Ile Asn Ile Leu Glu Asp Trp Asn His Ala Asp Pro Glu Tyr Phe Asn
1060 1065 1070

Lys Ile Gly Asn Pro Gln Leu Thr Met Asp Asp Thr Ile Lys Asn Ser
1075 1080 1085

Leu Asn His Gly Leu Ser Asp Ala Thr Asn Arg Trp Gly Leu Asp Ala
1090 1095 1100

Ile Val His Gln Ser Leu Ala Asp Arg Glu Asn Asn Ser Thr Glu Asn
1105 1110 1115 1120

Val Val Ile Pro Asn Tyr Ser Phe Val Arg Ala His Asp Asn Asn Ser
1125 1130 1135

Gln Asp Gln Ile Gln Asn Ala Ile Arg Asp Val Thr Gly Lys Asp Tyr
1140 1145 1150

His Thr Phe Thr Phe Glu Asp Glu Gln Lys Gly Ile Asp Ala Tyr Ile
1155 1160 1165

Gln Asp Gln Asn Ser Thr Val Lys Lys Tyr Asn Leu Tyr Asn Ile Pro
1170 1175 1180

Ala Ser Tyr Ala Ile Leu Leu Thr Asn Lys Asp Thr Ile Pro Arg Val

185	1190	1195	1200
Tyr Tyr Gly Asp Leu Tyr Thr Asp Gly Gly Gln Tyr Met Glu His Gln	1205	1210	1215
Thr Arg Tyr Tyr Asp Thr Leu Thr Asn Leu Leu Lys Ser Arg Val Lys	1220	1225	1230
Tyr Val Ala Gly Gly Gln Ser Met Gln Thr Met Ser Val Gly Gly Asn	1235	1240	1245
Asn Asn Ile Leu Thr Ser Val Arg Tyr Gly Lys Gly Ala Met Thr Ala	1250	1255	1260
Thr Asp Thr Gly Thr Asp Glu Thr Arg Thr Gln Gly Ile Gly Val Val	1265	1270	1275
Val Ser Asn Thr Pro Asn Leu Lys Leu Gly Val Asn Asp Lys Val Val	1285	1290	1295
Leu His Met Gly Ala Ala His Lys Asn Gln Gln Tyr Arg Ala Ala Val	1300	1305	1310
Leu Thr Thr Thr Asp Gly Val Ile Asn Tyr Thr Ser Asp Gln Gly Ala	1315	1320	1325
Pro Val Ala Met Thr Asp Glu Asn Gly Asp Leu Tyr Leu Ser Ser His	1330	1335	1340
Asn Leu Val Val Asn Gly Lys Glu Glu Ala Asp Thr Ala Val Gln Gly	1345	1350	1355
Tyr Ala Asn Pro Asp Val Ser Gly Tyr Leu Ala Val Trp Val Pro Val	1365	1370	1375
Gly Ala Ser Asp Asn Gln Asp Ala Arg Thr Ala Pro Ser Thr Glu Lys	1380	1385	1390
Asn Ser Gly Asn Ser Ala Tyr Arg Thr Asn Ala Ala Phe Asp Ser Asn	1395	1400	1405
Val Ile Phe Glu Ala Phe Ser Asn Phe Val Tyr Thr Pro Thr Lys Glu	1410	1415	1420
Ser Glu Arg Ala Asn Val Arg Ile Ala Gln Asn Ala Asp Phe Phe Ala	1425	1430	1435
Ser Leu Gly Phe Thr Ser Phe Glu Met Ala Pro Gln Tyr Asn Ser Ser	1445	1450	1455
Lys Asp Arg Thr Phe Leu Asp Ser Thr Ile Asp Asn Gly Tyr Ala Phe	1460	1465	1470
Thr Asp Arg Tyr Asp Leu Gly Met Ser Glu Pro Asn Lys Tyr Gly Thr	1475	1480	1485
Asp Glu Asp Leu Arg Asn Ala Ile Gln Ala Leu His Lys Ala Gly Leu			

1490

1495

1500

Gln Val Met Ala Asp Trp Val Pro Asp Gln Ile Tyr Asn Leu Pro Gly
505 1510 1515 1520

Lys Glu Val Ala Thr Val Thr Arg Val Asp Asp Arg Gly Asn Val Trp
1525 1530 1535

Lys Asp Ala Ile Ile Asn Asn Asn Leu Tyr Val Val Asn Thr Ile Gly
1540 1545 1550

Gly Gly Glu Tyr Gln Lys Lys Tyr Gly Gly Ala Phe Leu Asp Lys Leu
1555 1560 1565

Gln Lys Leu Tyr Pro Glu Ile Phe Thr Lys Lys Gln Val Ser Thr Gly
1570 1575 1580

Val Ala Ile Asp Pro Ser Gln Lys Ile Thr Glu Trp Ser Ala Lys Tyr
585 1590 1595 1600

Phe Asn Gly Thr Asn Ile Leu His Arg Gly Ser Gly Tyr Val Leu Lys
1605 1610 1615

Ala Asp Gly Gly Gln Tyr Tyr Asn Leu Gly Thr Thr Thr Lys Gln Phe
1620 1625 1630

Leu Pro Ile Gln Leu Thr Gly Glu Lys Lys Gln Gly Asn Glu Gly Phe
1635 1640 1645

Val Lys Gly Asn Asp Gly Asn Tyr Tyr Phe Tyr Asp Leu Ala Gly Asn
1650 1655 1660

Met Val Lys Asn Thr Phe Ile Glu Asp Ser Val Gly Asn Trp Tyr Phe
665 1670 1675 1680

Phe Asp Gln Asp Gly Lys Met Val Glu Asn Lys His Phe Val Asp Val
1685 1690 1695

Asp Ser Tyr Gly Glu Lys Gly Thr Tyr Phe Phe Leu Lys Asn Gly Val
1700 1705 1710

Ser Phe Arg Gly Gly Leu Val Gln Thr Asp Asn Gly Thr Tyr Tyr Phe
1715 1720 1725

Asp Asn Tyr Gly Lys Met Val Arg Asn Gln Thr Ile Asn Ala Gly Ala
1730 1735 1740

Met Ile Tyr Thr Leu Asp Glu Asn Gly Lys Leu Ile Lys Ala Ser Tyr
745 1750 1755 1760

Asn Ser Asp Ala Glu Tyr Pro Thr Ser Thr Asp Val Gly Lys Met Leu
1765 1770 1775

Asp Gln Asn Lys Leu
1780

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<213> Lactobacillus reuteri

<220>
<221> REPEAT
<222> (1)..(13)

<400> 3
Tyr Tyr Phe Tyr Asp Leu Ala Gly Asn Met Val Lys Asn
1 5 10

<210> 4
<211> 13
<212> PRT
<213> Lactobacillus reuteri

<220>
<221> REPEAT
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Trp Tyr Phe Phe Asp Gln Asp Gly Lys Met Val Glu Asn
1 5 10

<210> 5
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<212> PRT
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<220>
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<400> 5
Thr Tyr Tyr Phe Asp Asn Tyr Gly Lys Met Val Arg Asn
1 5 10

<210> 6
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
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primer GTFpr1

<400> 6
gayaakwsna aksynrtngt nsargc

26

<210> 7
<211> 22
<212> DNA
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<220>
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primer GTFpr2

<400> 7
gnkcncanat ratrcnctr na

22

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<211> 35
<212> DNA
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<220>
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primer GTFpr3

<400> 8
acaaccacca tggaattagg tcgcactgat gtaac

35

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<212> DNA
<213> Artificial Sequence

<220>
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primer GTFpr4

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47